

GAP of: 0964sid4 check: 9188 from: 1 to: 368

WPDEF Case 0964 Rad23 SEQ ID NO: 4 corn

Case 0964 Rad23 SEQ ID NO: 4 corn

to: 0964DY12013aa check: 506 from: 1 to: 382

WPDEF Case 0964D Rad23 protein encoded by GenBank Y12013 carrot

Case 0964D Rad23 protein encoded by GenBank Y12013 carrot

Y12013. Daucus carota mRNA. . .[gi:1914682] Links

LOCUS DCRAD23I 1496 bp mRNA linear PLN 28-JAN-1999

DEFINITION Daucus carota mRNA for RAD23 protein, isoform I.

ACCESSION Y12013 . . .

Symbol comparison table: /app/gcg/10.2/gcgcore/data/rundata/blosum62.cmp

CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad.
Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778
Length Weight: 2 Average Mismatch: -2.248

Quality: 922 Length: 389
Ratio: 2.505 Gaps: 10
Percent Similarity: 63.989 Percent Identity: 56.787

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

0964sid4 x 0964DY12013aa March 31, 2003 14:18 ..

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      .
1 MKLTVKTLKGTHFEIRVQPNDTIMAVKKNIEEIQ GKDSYPWGQQLLIFNG 50
  ||: |||||. |||. | |. |.: ||: . || || ||: ||: |
1 MKIYVKTLKGSQFEIQVNPDDSVADV KRSIETAQGA AVYPAAQQMLIYQG 50
      .
51 KVLKDESTLEENKVNEDGFLVVMLSKGKTSGSTG..TSSSQHSNTPATRQ 98
  ||||| . || || | |. | : | : |||| |. | ||.. | |
51 KVLKDGTTLLENNVAENSFIVIMLSKSKSPSGEGSTTSTAAAPKAPQ TSA 100
      .
99 APPLEAPQQAPQPPVA..PITTSQPEGLPAQAP.....NTHDNAA 136
  | . || || | |. | : | | || || | : |. ||
101 PPSVPAP.AVSQPPASTLPVPAPSPAPAPATAPIPSAAVGSEANVYDSAA 149
      .
137 SNLLSGRNVDTIINQLMEMGGGSWDKDKVQRALRAAYNNPERAVEYLYSG 186
  | |.. | |. | | : : |||| | : | | | . ||| : ||||| |||||
150 SLLVAGSNLEGA IQQILDMGGGTWDRDTVIRIVRAAFNNPERAVEYLYSG 199
      .
187 IPVTAE...IA.VPIGGQGANTTDRAPTG..EAGLSGIPNTAPLDLFPQG 230
  || || : | | || || |. | | | || |||||
200 IPEQAEAPPVAPSPPSGQAANPLDQPPAAAQ PAPASAGPNANPLDLFPQG 249
      .

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231 ASNAG.GGAGGGPLDFLRNNPQFQAVREMVHTNPQILQPMLVELSKQNPQ 279
    . | || | |||| | ||||. | | . ||||| || ||||
250 LPDMGSNAAGAGNLDFLRTNQFQALRAMVQSNPQILQPMLQELGKQNPH 299
    . . . . .
280 ILRLIEENHDEFLQLLNEPFEGGEGDFLDQPEEDEMPHAISVTPEEQEAI 329
    ::|||:|. :|||:| | | | . | | |||||.:||
300 LMRLIQEHQADFLQLINEPMEGGE.NLLGHG.....PQAISVTPEERDAI 343
    . . . . .
330 GRLESMGFDRARVIEAFLACDRNEELAANYLLEHAGEED 368
    |||.|||| |:| | | |.:|||||:|| | :
344 ERLEAMGFDRELVLEVFFACNKNEELAANYLLDHMHEFE 382

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